## AMENDMENTS TO THE SPECIFICATION

Amend the paragraph beginning at page 117, line 14, as follows:

PCR preparation and conditions included the following steps: Sample RNA from each tissue (poly A+ RNA, 2.8 pg) and the cell lines (total RNA, 70 ng) was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). A panel of 41 normal human tissues and 55 human cancer cell lines was employed (see Table ~~6~~ 3).

Amend the paragraph beginning at page 123, line 8, as follows:

It was observed that in certain experiments treatment with the vector pCEP4/Sec/30664188.m99 did not result in DNA synthesis or cell proliferation. In additional experiments, medium conditioned with 30664188.m99 was obtained from HEK 293 cells grown in the presence of serum (Example 6). The 30664188.m99 gene product was purified by cation exchange chromatography, followed by nickel affinity chromatography. The protein product was run under nonreducing and reducing conditions on SDS-PAGE, and developed by Coomassie stain. The results are shown in FIGS. 10A and 10B. In the presence of serum, the 30664188.m99 gene product appeared as a protein of about 35 kDa under nonreducing conditions (FIG. 10B). However, this polypeptide appears as three degraded bands when run under reducing conditions. The apparent molecular weights of the ~~two~~ three bands were 22-25 kDa (band I), about 16 kDa (band II) and about 5-6 kDa (band III). N-terminal amino acid analysis of these fragments indicates that bands I and II both begin at residue 247 of the 30664188.m99 amino acid sequence, and that band III begins at residue 339. These results are consistent with cleavage of the polypeptide corresponding to band I to provide the fragments of bands II and III. It is possible that the 35 kDa band observed under nonreducing conditions is a dimer composed of band I, and/or the bonded polypeptide composed of bands II and III, observed under reducing conditions.